The Ultimate AP® Biology Unit 7 Cheat Sheet

7.1–7.3 Natural & Artificial Selection

Darwin's Logic (VISTA)

Variation: individuals differ in heritable traits (variation arises from mutation, meiosis & sexual reproduction).
Overproduction: more offspring born than can survive → competition for limited resources (food, mates).
Selection: individuals w/ advantageous traits survive & reproduce more → **differential reproductive success**.
Time + Adaptation: favorable alleles ↑ in frequency over many generations → the population adapts.

Key Ideas

Fitness = reproductive success (# of fertile offspring left behind), NOT strength, size or lifespan.
Selection acts on phenotypes, but populations evolve (allele freq. Δ); single individuals never evolve.
Environment decides which trait is favored; changing env. → changing selection (dark peppered moths in sooty forests, Galápagos finch beaks in drought years).
Biotic (predators, competitors, parasites) & **abiotic** (climate, water, temp., pH) factors both drive selection.

Artificial Selection

	Natural	Artificial
Selector	Environment	Humans
Goal	None	Desired traits
Examples	Antibiotic resist.	Dogs, corn, brassica

Brassica oleracea → cabbage, broccoli, kale, cauliflower: all 1 species, w/ diff. traits selected by farmers.
Convergent evolution: similar env. pressures → similar traits in unrelated groups (shark & dolphin shape).

⚠ Organisms don't evolve "because they need to". Variation exists first; selection sorts it.

✓ FRQ chain: variation → selective pressure → differential survival/reproduction → allele freq. Δ.

7.4 Population Genetics

Evolution = Allele Frequency Change

Gene pool: all alleles in a population. **Microevolution**: Δ in allele frequencies in a pop. over generations.

Mechanism	Effect	Adaptive?
Natural sel.	Favors fit alleles	Yes
Genetic drift	Random Δ	No
Gene flow	Mixes pops	No
Mutation	New alleles	No
Nonrandom mating	Genotype Δ	No

Genetic Drift

Drift: chance events change allele freq.; strongest in **small populations**; can lose or fix alleles at random.
Bottleneck: disaster cuts pop. size → survivors' alleles by chance (cheetahs, northern elephant seals).
Founder effect: small group starts a new pop. → unusual allele freq. by chance (e.g., Amish polydactyly).

Modes of Selection

Directional: one extreme favored → the whole curve shifts that way (e.g., bigger finch beaks in drought).
Stabilizing: middle favored → curve narrows as both extremes are lost (e.g., human birth weight).
Disruptive: both extremes favored → 2 peaks (hard & soft seeds only → small & large beaks, few medium).
Sexual selection: mate choice & male–male competition → showy traits (peacock tails), even if costly to survival.
Gene flow: migration moves alleles between pops → pops become more alike; can also add new variation.

⚠ Drift is RANDOM, not adaptive. Natural selection is the only mechanism that consistently adapts.

✓ Graph Q: compare before/after curves. Shift → directional; narrow → stabilizing; split → disruptive.

7.5 Hardy-Weinberg Equilibrium

Equations (Formula Sheet)

Alleles: p + q = 1 (p = dominant allele freq., q = recessive).
Genotypes: $p^2 + 2pq + q^2 = 1$ (p^2 = AA, 2pq = Aa, q^2 = aa).

5 Conditions (No Evolution)

1) Large population (no drift) **2)** No migration **3)** No mutation **4)** Random mating **5)** No natural selection.
Real pops rarely meet all 5 → HW is a null model; deviation from it means evolution is happening.
Violated condition → mechanism: small pop → drift; migration → gene flow; selection → adaptation.

Solving Problems

Start w/ q^2: recessive phenotype freq. = q^2 (the only genotype you can see directly). Then $q = \sqrt{q^2}$.
Worked: 16% white (aa) → $q^2 = 0.16$ → q = 0.4 → p = 0.6. AA = 0.36, Aa = 2(0.6)(0.4) = 0.48, aa = 0.16.
Counts: in 500 plants → AA = 180, Aa = 240, aa = 80.
Next gen. (if HW holds): p & q stay 0.6 & 0.4 → same genotype frequencies every generation.

Given	Find first
% recessive phenotype	$q = \sqrt{(q^2)}$
% dominant phenotype	$q^2 = 1 - $ that
Genotype counts	Count alleles

Counting alleles: 40 AA, 40 Aa, 20 aa = 100 people → 200 alleles; p = (2·40 + 40)/200 = 0.6, so q = 0.4.
Test for evolution: compare observed genotype counts to HW expected counts using χ^2 (Unit 5 steps).
Carriers (2pq) of a rare recessive disease are far more common than affected people (q^2) in a population.
Sex-linked: male phenotype freq. = allele freq. (% affected males = q for an X-linked recessive trait, b/c 1 X).

⚠ Never take √ of the DOMINANT phenotype %. It includes both AA and Aa. Always start from q^2.

✓ Check: p + q = 1 and $p^2 + 2pq + q^2 = 1$. If either sum is off, go back and recheck your square roots.

7.6–7.8 Evidence & Common Ancestry

Evidence of Evolution

Type	Example
Fossils	Whale ancestors w/ legs
Homologous struct.	Human arm, bat wing
Vestigial struct.	Whale pelvis
Molecular	DNA, protein seq.
Embryology	Pharyngeal pouches
Biogeography	Island species

Homologous = same origin, diff. function → common ancestry (divergent). **Analogous** = same function, diff. origin → convergent evolution (bird & insect wings).
Fossil dating: relative (rock layers; deeper = older) & radiometric (isotope half-life → absolute age in years).
Transitional fossils: *Tiktaalik* (fish → tetrapod), *Archaeopteryx* (dinosaur → bird), whales w/ legs.

7.7 Common Ancestry

All life shares: DNA/RNA, the genetic code, ribosomes, glycolysis, ATP, cell membranes → 1 common origin.
Eukaryotes share: membrane-bound organelles, linear chromosomes, introns in genes → 1 eukaryote ancestor.
Fewer DNA or amino acid sequence differences between 2 species → a more recent common ancestor.
Cytochrome c: human vs chimp 0 amino acid differences; human vs yeast ~44 → chimp is much more closely related.

7.8 Continuing Evolution

Antibiotic resistance: resistant bacteria survive treatment → reproduce → resistant pop. Same for pesticides, HIV drugs.
Evolution is ongoing; all species alive today are still evolving.

⚠ Antibiotics don't CAUSE resistance mutations. They select for ones that are already present.

✓ Homologous → common ancestor. Analogous → similar environment & pressures, not close relatedness.

7.9 Phylogeny

Reading Trees

Phylogenetic tree: hypothesis of evolutionary relationships.
Cladogram: branching order only (no time scale).
Node = common ancestor where a lineage splits. **Tips** = living (or extinct) taxa. **Root** = oldest common ancestor.
Sister taxa: share the most recent common ancestor w/ each other → they are each other's closest relatives.
Relatedness: trace back to the most recent shared node, NOT the distance between the tips on the page.
Nodes rotate: swapping the branches at any node doesn't change any of the relationships the tree shows.
Branch length (if scaled) = time or amount of genetic change; unscaled trees show branching order only.

Building Trees

Shared derived characters: traits new to a group → define clades (e.g., hair & milk → mammals only).
Outgroup: related group just outside the ingroup → shows which traits are the ancestral ones (pre-split).
Parsimony: best tree = fewest evolutionary changes.
Molecular data (DNA, amino acids) usually more reliable than morphology; trees updated as data grow.

Trait →	Lamprey	Frog	Lizard	Mouse
Jaws	–	+	+	+
4 limbs	–	+	+	+
Amnion	–	–	+	+
Hair	–	–	–	+

Clade (monophyletic) = ancestor + ALL its descendants.
Paraphyletic = an ancestor + only some of its descendants (e.g., "reptiles" w/o birds). Not a true clade.
Trees support: birds are dinosaurs; whales closest to hippos.

⚠ Taxa next to each other at the tips aren't always closest relatives. Follow the branches back to the nodes.

✓ Character table → count the + marks for each taxon; more shared derived traits = closer together on the tree.

7.10 Speciation

What Is a Species

Biological species concept: can interbreed in nature → fertile offspring. Doesn't work for fossils or asexual orgs.
Other concepts: morphological (form), ecological (niche), phylogenetic (shared ancestry from DNA data).

Reproductive Isolation

Prezygotic	Example
Habitat	Water vs land snakes
Temporal	Diff. breeding season
Behavioral	Diff. mating songs
Mechanical	Parts don't fit
Gametic	Sperm can't bind egg

Postzygotic: hybrid inviability, hybrid sterility (mule), hybrid breakdown (2nd-generation hybrids weak or sterile).

Modes

Allopatric: geographic barrier → pops diverge (Kaibab & Abert squirrels on either side of the Grand Canyon).
Sympatric: same area; via polyploidy (plants), habitat use or mate choice (e.g., cichlid fish in one African lake).
Polyploidy: meiosis error → 4n plant can't breed w/ 2n parent → new species in 1 generation.
Adaptive radiation: one ancestor → many species filling diff. niches (Darwin's finches, Hawaiian honeycreepers).

Tempo

Gradualism: slow, steady Δ over time. **Punctuated equilibrium**: long stasis broken by rapid bursts of change.
Hybrid zones: where 2 species meet & mate; outcomes are reinforcement (barriers strengthen), fusion, or stability.

⚠ Mules are hybrids, not a species. They're sterile → a classic example of a postzygotic barrier.

✓ Speciation Q: name the barrier, say prezygotic or postzygotic, and explain exactly how gene flow stops.

7.11–7.12 Extinction & Variation

7.11 Extinction

Background extinction: normal, ongoing rate. **Mass extinction**: many groups lost fast (5 major events).
Causes: climate Δ, asteroid impact (end-Cretaceous, non-avian dinosaurs), volcanism, habitat loss, invasive species, human activity (overhunting, pollution).
After mass extinction: open niches → **adaptive radiation** (e.g., mammals diversified after the dinosaurs).
Human impact: habitat destruction, overhunting, pollution → current extinction rate ↑ far above background.
Rate of speciation vs extinction sets biodiversity over time.
Ecosystem effect: losing just one keystone species can collapse a whole community & food web (Unit 8).

7.12 Variation in Populations

Genetic diversity: more alleles → better odds some individuals survive an env. change or new disease.
Low diversity → vulnerable: Irish potato famine (all clones, all susceptible), cheetahs, Florida panthers.

Pop. trait	Response to change
High diversity	Some survive → adapt
Low diversity	All at risk → decline
Small size	Drift, inbreeding ↑

Fix: gene flow from other pops (Texas pumas → Florida panthers) restored their diversity & health.
Heterozygote advantage: Aa favored (sickle cell allele + malaria) → keeps both alleles in the population.
Bacteria: huge pops + fast generations + gene sharing (plasmids) → high diversity → adapt very quickly.
Conservation: protect genetic diversity w/ habitat corridors, seed banks, captive breeding programs.

⚠ Variation must exist BEFORE the change. A uniform population can't adapt in time to survive.

✓ FRQ: link low genetic diversity → fewer resistant individuals → higher extinction risk for the pop.

7.13 Origin of Life & Exam Strategy

Timeline

Earth ~4.6 bya. **First life** ~3.5–3.9 bya (prokaryotes, stromatolites). First eukaryotes ~1.8–2 bya.
Early atmosphere: reducing; little/no free O_2. Energy for reactions came from lightning, UV, volcanoes.
Evidence: oldest fossils = stromatolites (cyanobacteria mats); O_2 rose ~2.4 bya (Great Oxidation Event).

Steps to Life

1) Abiotic synthesis of monomers (Miller–Urey: amino acids formed from simple gases + electric sparks).
2) Polymers form (on clay or hot surfaces). **3) Protocells**: lipid bubbles enclose these molecules, keep them close.
4) Self-replication: **RNA world** hypothesis: early RNA stored info AND catalyzed reactions (ribozymes).
Why RNA first: it can be both gene & enzyme; the ribosome's catalytic core is still made of RNA today.
Alternatives: deep-sea hydrothermal vents as the cradle; organic molecules delivered by meteorites.

Exam Moves

Selection FRQ: name the trait, the pressure, who survives/reproduces, and the Δ in allele freq.
HW math: always start from q^2; show p, q and genotype freq.
Tree Qs: use the nodes, not tip order; justify w/ shared derived traits or DNA/protein sequence data.
Links: Unit 5 alleles & χ^2, Unit 6 mutation as the source of variation, Unit 8 populations & ecosystems.
Data Qs: read graphs of allele freq. over time; a steady trend → selection; a random wobble → genetic drift.
Justify w/ evidence: cite fossils, homologous structures or sequence data, never opinion or "need".

⚠ Use "population evolves" and "allele frequency changes", never "the individual adapts".

✓ Every evolution answer needs heritable variation + differential survival & reproduction over generations.